

CLAIMS

1. A peptide, characterized in that it has a helix-loop-helix type structure comprising the sequence of a calmodulin loop including at least one mutation to neutral residues selected from the group consisting of Ser (S), Thr (T), Cys (C), His (H), Tyr (Y), Asn (N) and Gln (Q), of one, two or three residues of at least one of the four calcium-binding sites of calmodulin:

. site I: residues selected from residues D20, D22 and D24,  
. site II: residues selected from residues D56, D58 and N60,  
. site III: residues selected from residues D93, D95 and N97,  
. site IV: residues selected from residues D129, D131 and D133,  
said positions being indicated with reference to the human calmodulin sequence (SWISSPROT P02593).

2. The peptide as claimed in claim 1, characterized in that the mutation is preferably a mutation to threonine (Thr), serine (Ser) or asparagine (Asn) neutral residues.

3. The peptide as claimed in claim 1 or claim 2, characterized in that the mutation is preferably a mutation, to a threonine residue, of residue D20, D22 or D24, a mutation, to a threonine, serine or asparagine residue, of the two residues D20 and D24, of the two residues D20 and D22 or of the two residues D22 and D24, or a mutation, to a threonine, serine or asparagine residue, of the three residues D20, D22 and D24.

4. The peptide as claimed in any one of claims 1 to 3, characterized in that it is a calmodulin calcium-binding site mutant.

5. The peptide as claimed in any one of claims 1 to 4, characterized in that it is a cyclic

peptide which has helices that each include a mutation of an amino acid residue to a residue that allows chemical bridging, in particular a cysteine residue, which cysteines are connected via a disulfide bridge.

5               6. The peptide as claimed in claim 5, characterized in that it has the mutations F19C and V35C.

10              7. The peptide as claimed in any one of claims 1 to 6, characterized in that it also includes the mutation of an amino acid residue to a fluorescent amino acid residue.

8. The peptide as claimed in claim 7, characterized in that said fluorescent amino acid residue is a tyrosine residue or a tryptophan residue.

15              9. The peptide as claimed in claim 8, characterized in that it has a mutation selected from the group consisting of: T26Y, T26W, A15W and F16W.

20              10. The peptide as claimed in any one of claims 1 to 9, characterized in that it has one of the sequences SEQ ID Nos. 4-7 or SEQ ID Nos. 9-12.

11. The peptide as claimed in any one of claims 1 to 10, characterized in that it is conjugated to at least one fluorophore.

25              12. The peptide as claimed in claim 11, characterized in that it is conjugated to two different fluorophores.

30              13. The peptide as claimed in claim 11 or claim 12, characterized in that said fluorophore is a fluorescent protein selected from: EBFP, ECFP, EYFP, EGFP, DsRed, CopGFP and PhiYFP.

14. The peptide as claimed in claim 11 or claim 12, characterized in that said fluorophore is selected from dansyl, coumarin, fluorescein and Alexa derivatives.

35              15. The peptide as claimed in any one of claims 1 to 14, characterized in that it is associated with at least one molecule that allows targeting to the kidney and/or to the bone.

16. The peptide as claimed in any one of

claims 1 to 14, characterized in that it is associated with a molecule that promotes its excretion *in vivo*.

17. A polypeptide, characterized in that it comprises the concatenation of at least two identical or different peptides as claimed in any one of claims 1 to 16.

18. A peptide composition, characterized in that it comprises at least one polypeptide as claimed in claim 17 and at least one suitable vehicle.

19. A fusion protein, characterized in that it consists of the in-frame fusion of the sequence of at least one peptide as claimed in any one of claims 1 to 10, with the sequence of an appropriate protein.

20. The fusion protein as claimed in claim 19, characterized in that the sequence of said peptide is fused to the sequence of a protein selected from the group consisting of calmodulin, chameleon proteins derived from the latter and proteins having a helix-loop-helix type motif, capable of binding calcium.

21. The fusion protein as claimed in claim 19 or claim 20, characterized in that it is conjugated to at least one fluorophore as defined in claim 13 or 14.

22. The fusion protein as claimed in claim 21, characterized in that one of the ends of said protein is coupled to a fluorescence donor, and the other is coupled to a fluorescence acceptor.

23. The fusion protein as claimed in claim 22, characterized in that it comprises, at one of its ends, the sequence of EBFP or ECFP and, at the other end, the sequence of EGFP or of EYFP.

24. The use of a product selected from the group consisting of: a peptide as claimed in any one of claims 1 to 16, a polypeptide as claimed in claim 17, a peptide composition as claimed in claim 18 and a fusion protein as claimed in any one of claims 19 to 23, for preparing a reagent for detecting soils and water contaminated with uranium.

25. The use of a product selected from the group consisting of: a peptide as claimed in any one of claims 1 to 16, a polypeptide as claimed in claim 17, a peptide composition as claimed in claim 18 and a fusion protein as claimed in any one of claims 19 to 23, for preparing a reagent for diagnosing individuals contaminated with uranium.

26. An isolated nucleic acid molecule, characterized in that it comprises a sequence encoding a peptide as claimed in any one of claims 1 to 16, a polypeptide as claimed in claim 17 or a fusion protein as claimed in any one of claims 19 to 23.

27. Probes and primers, characterized in that they are capable of specifically detecting/ amplifying the nucleic acid molecules as claimed in claim 26, which probes and primers comprise a sequence of approximately 10 to 30 nucleotides that is adjacent to a helix-loop-helix type motif or else to one of the helices or to the loop of this motif, of a calcium ion-binding protein.

28. A eukaryotic or prokaryotic recombinant vector, characterized in that it comprises an insert consisting of a nucleic acid molecule as claimed in claim 26.

29. Eukaryotic or prokaryotic cells, characterized in that they are modified with a recombinant vector as claimed in claim 28.

30. A transgenic nonhuman animal organism, characterized in that it comprises cells modified with a nucleic acid molecule as claimed in claim 26.

31. A transgenic plant, characterized in that it comprises cells modified with a nucleic acid molecule as claimed in claim 26.

32. Prokaryotic or eukaryotic cells modified with a regulatory system that includes a peptide as claimed in any one of claims 1 to 16 as a regulator or repressor of a gene encoding a bioluminescent protein.

33. The use of the modified prokaryotic or eukaryotic cells as claimed in claim 29 or of

transgenic plants as claimed in claim 31, for the remediation of soils and water contaminated with uranium.

5       34. The use of the modified prokaryotic or eukaryotic cells as claimed in claim 32, for preparing a reagent for detecting soils and water contaminated with uranium.

10       35. The use of the modified prokaryotic or eukaryotic cells as claimed in claim 32, for preparing a reagent for diagnosing individuals contaminated with uranium.

36. An antibody, characterized in that it binds selectively to the peptide as claimed in any one of claims 1 to 16.

15       37. A kit for detecting a contamination with uranium, characterized in that it comprises at least: a peptide as claimed in any one of claims 1 to 16, a polypeptide as claimed in claim 17, a peptide composition as claimed in claim 18, a fusion protein as  
20       claimed in any one of claims 19 to 23, an antibody as claimed in claim 36, or modified prokaryotic or eukaryotic cells as claimed in claim 32.